Spread of Infectious Diseases with a Latent Period

Kanako Mizuno, Kazue Kudo

Abstract Infectious diseases spread through human networks. Susceptible-Infected-Removed (SIR) model is one of the epidemic models to describe infection dynamics on a complex network connecting individuals. In the metapopulation SIR model, each node represents a population (group) which has many individuals. In this paper, we propose a modified metapopulation SIR model in which a latent period is taken into account. We call it SIIR model. We divide the infection period into two stages: an infected stage, which is the same as the previous model, and a seriously ill stage, in which individuals are infected and cannot move to the other populations. The two infectious stages in our modified metapopulation SIR model produce a discontinuous final size distribution. Individuals in the infected stage spread the disease like individuals in the seriously ill stage and never recover directly, which makes an effective recovery rate smaller than the given recovery rate.

1 Introduction

Infectious diseases spread through human networks. Susceptible-Infected-Removed (SIR) model is one of the epidemic models to describe infection dynamics on a complex network connecting individuals. The ratio of the transmission rate to the recovery rate is called the basic reproduction number R_0. It is the expected number of infections caused by a typical infectious individual in a completely susceptible population [1, 2]. In the standard SIR model, the outbreak occurs when $R_0 > 1$.

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The likely magnitude of the outbreak, which is called the expected final size of the epidemic, depends only on R_0 [2, 3].

The spread of infectious diseases also depends on human mobility. In metapopulation SIR models, movements between different populations (groups) are taken into account [4, 5, 6]. Each node of the metapopulation network represents a group of individuals. Individuals can move between two nodes connected by a link. Although the epidemic threshold is R_0 in each group, the global invasion threshold in the metapopulation system depends on the mobility rate as well as its network structure [5, 6].

In this paper, we propose a modified metapopulation SIR model in which a latent period is taken into account. Infected individuals behave like susceptible ones when they do not feel sick. They move between linked populations and spread diseases across different populations. We consider that such infected individuals are in a latent period. We assume that infected individuals become too sick to move after the latent period. Such ill individuals infect only the susceptible ones in the same population. This model is different from the SEIR model [7], which is a common epidemic model in which a latent period is incorporated as an "Exposed" state. However, it belongs to a family of generalized SIR models that include multiple infectious stages [2]. The two infectious stages in our modified metapopulation SIR model produce a discontinuous final size distribution with a jump at $R_0 = 1$.

The rest of the paper is organized as follows. The metapopulation SIR model and the modified SIR model are introduced in Sec. 2. We demonstrate the discontinuous final size distribution of the modified model in Sec. 3. The effective recovery rate, which is different from the given recovery rate, is estimated, and it is the key to find what causes the discontinuity. Discussions and conclusions are given in Sec. 4.

2 Model

First we introduce a metapopulation SIR model, which is an SIR model that is extended to metapopulation networks. In the metapopulation SIR model, each node represents a population (group) which has many individuals, and each individual is in one of three states: S (susceptible), I (infected) or R (recovered). Individuals of state S are infected by those of state I in the same population. The infection rate is given by $\alpha I_m/N_m$, where $N_m = S_m + I_m + R_m$ with S_m, I_m, and R_m being the number of susceptible, infected, and recovered individuals of population m, respectively. In other words, the rate that S becomes I depends on the transmission rate α and the proportion of I in the same population. The constant rate that I becomes R, i.e., recovery rate, is defined as β. We here assume that all individuals move between the populations connected with links in the network at a constant rate w. The travel rate w is the same for all the individuals. The time evolution of the numbers of S, I and R in each population is described by

$$\partial_t S_n = -\alpha S_n I_n / N_n + w \sum_m (S_m - S_n), \tag{1a}$$

$$\partial_t I_n = \alpha S_n I_n / N_n - \beta I_n + w \sum_m (I_m - I_n), \tag{1b}$$

$$\partial_t R_n = \beta I_n + w \sum_m (R_m - R_n), \tag{1c}$$

where the summations are taken over all the populations connected with population n.

Next, we divide the infection period into two stages: an infected stage, which is the same as the previous model, and a seriously ill stage, in which individuals are infected and cannot move to the other populations. We call this model SIIR model. In this model, each individual is in one state of S (susceptible), H (infected), I (seriously ill), and R (recovered). Individuals of S in population m are infected and become H at rate $\alpha(H_m + I_m)/N_m$, where $N_m = S_m + H_m + I_m + R_m$. Individuals of H become I at a constant rate μ. Individuals of I recover and become R at a rate β. In the SIIR model, individuals of H move between the populations connected with links at a rate w, however, individuals of I do not. The time evolution of the numbers of S, H, I and R in each population is described by

$$\partial_t S_n = -\alpha S_n (H_n + I_n)/N_n + w \sum_m (S_m - S_n), \tag{2a}$$

$$\partial_t H_n = \alpha S_n (H_n + I_n)/N_n - \mu H_n + w \sum_m (H_m - H_n), \tag{2b}$$

$$\partial_t I_n = \mu H_n - \beta I_n, \tag{2c}$$

$$\partial_t R_n = \beta I_n + w \sum_m (R_m - R_n), \tag{2d}$$

where the summations are taken over all the populations connected with population n.

3 Final Size Distribution

The spread of a disease is expressed by attack ratio, which is the final proportion of R when I disappears in the entire metapopulation. The attack ratio plotted as the function of the basic reproduction number α/β is called a final size distribution. The final size distributions of the SIR model and SIIR models are shown in Fig. 1. In this simulation, the number of individuals in each state is taken as a real number and the time step is discrete. We use a scale-free network with 900 nodes, whose degree distribution is $P(k) \sim k^{-\gamma}$ with $\gamma = 2.5$. The essential results do not depend on *gamma*. In the initial state, 100 susceptible individuals belong to each node except for one randomly selected node in which one infected individual is included. The global invasion does not occur when $\alpha < \beta$ in the SIIR model as well as the SIR model. The change in attack ratio is continuous at $\alpha = \beta$ in the high-w region in the

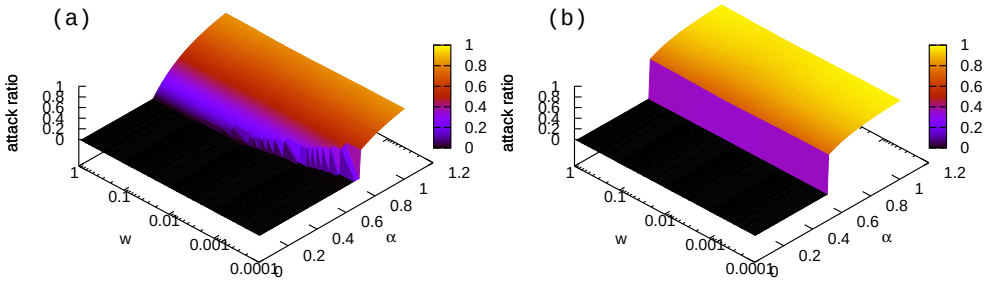

Fig. 1 Final size distributions of (a) metapopulation SIR model and (b) metapopulation SIIR model as the function of the transmission rate α and the travel rate w. In both cases, the recovery rate is $\beta = 0.5$.

SIR model, however, it is discontinuous in all region in the SIIR model. The shift of threshold in the low-w regions of the SIR model is often observed in metapopulation networks [5, 6].

In this paper, we focus on the discontinuous final size distribution of the SIIR model. The jump in the attack ratio arises from the difference between the given recovery rate and an effective recovery rate. In the SIIR model, individuals H spread the disease like individuals I and never become R directly. Therefore, the effective recovery rate β' is expected to be smaller than the given recovery rate β.

We show how to evaluate β' below. Disregarding traveling between populations, the SIIR model (2) is rewritten as

$$\partial_t S = -\alpha S(H+I), \tag{3a}$$
$$\partial_t H = \alpha S(H+I) - \mu H, \tag{3b}$$
$$\partial_t I = \mu H - \beta I, \tag{3c}$$
$$\partial_t R = \beta I, \tag{3d}$$

where $S = S_n/N_n$, $H = H_n/N_n$, $I = I_n/N_n$ and $R = R_n/N_n$. Combining Eqs. (3b) and (3c), we have

$$\partial_t(H+I) = \alpha S(H+I) - \beta'(H+I),$$
$$\beta' = \frac{I}{H+I}\beta.$$

We here take $\partial_t I = 0$, which leads to $H = (\beta/\mu)I$. Then, the effective recovery rate is calculated as

$$\beta' = \frac{\mu}{\beta+\mu}\beta. \tag{4}$$

Figure 2 illustrates that the evaluation of the effective recovery rate is appropriate. The simulation is performed in the same network with the same initial condition as

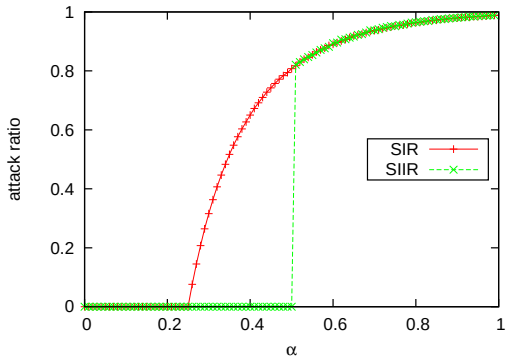

Fig. 2 The final size distribution as the function of the transmission rate α for the SIR model with the given recovery rate $\beta = 0.25$ is compared with that for the SIIR model with the effective recovery rate $\beta' = 0.25$, which is calculated from Eq. (4) with $\beta = 0.5$ and $\mu = 0.5$. Both curves agree in the region where $\alpha > 0.5$. The travel rate $w = 0.1$ for both curves.

Fig. 1. The travel rate is $w = 0.1$, which is in the high-w region. The attack ratio for the SIIR model is calculated for $\beta = 0.5$ and $\mu = 0.5$. In this case, the effective recovery rate is $\beta' = 0.25$. The final size distribution for the SIR model with the given recovery rate $\beta = 0.25$ agrees with that for the SIIR model in the region where $\alpha > 0.5$. This result implies the following. The effective recovery rate in the SIIR model is given by β', however, global invasion cannot occur when $\alpha < \beta$. The difference between β and β' causes the discontinuous final size distribution of the SIIR model.

Since we disregarded traveling between populations when we evaluate the effective recovery rate, the assumption that I is immobile should be irrelevant to the discontinuity in the final size distribution of the SIIR model. We now modify the SIIR model (2), replacing Eq. (2c) by

$$\partial_t I_n = \mu H_n - \beta I_n + w \sum_m (I_m - I_n). \tag{5}$$

Figure 3 shows the final size distribution of the modified SIIR model. The simulation is performed in the same conditions as Fig. 2. The profile of the SIIR curve in Fig. 2 looks the same as the curve in Fig. 3. Therefore, the cause of the discontinuous final size distribution is the division of the infection period into two stages, and the mobility of I has no effect on the discontinuity.

4 Discussions and Conclusions

The effective recovery rate β', which is given by Eq. (4), can be evaluated by another way. The basic reproduction number for the generalized SIR model that includes n infectious stages is given by

$$R_0 = \sum_{i=1}^{n} \frac{\alpha_i}{\beta_i}, \tag{6}$$

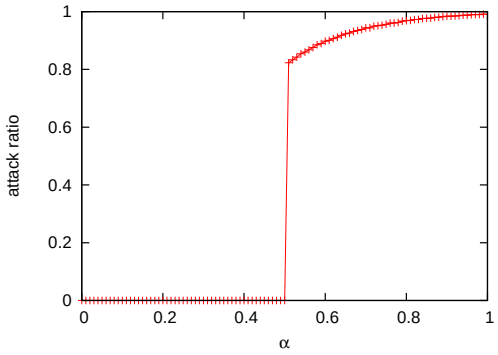

Fig. 3 The final size distribution of the modified SIIR model in which H moves between populations. α is the transmission rate. The travel rate $w = 0.1$.

where α_i is the transmission rate of the ith infectious stage, and $1/\beta_i$ is the mean duration of the stage [2, 8]. In our SIIR model, $\alpha_1 = \alpha_2 = \alpha$, $\beta_1 = \mu$ and $\beta_2 = \beta$, and thus, $R_0 = \alpha/\mu + \alpha/\beta = \alpha(\mu+\beta)/(\mu\beta)$. Therefore,

$$\beta' = \frac{\alpha}{R_0} = \frac{\mu\beta}{\mu+\beta}, \tag{7}$$

which is the same as Eq. (4).

In conclusion, the discontinuous final size distribution in the SIIR model is caused by the division of the infection period into two stages and the fact that the global invasion cannot occur when $\alpha < \beta$. The final size distribution depends on the effective recovery rate β', and its shape coincides with that of the SIR model with a recovery rate $\beta = \beta'$ in the region where $\alpha > \beta$.

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